

SEQ ID NO: 1

SEQUENCE TYPE: nucleic acid

**TOPOLOGY:** linear

HYPOTHETICAL: No

10 ORIGINAL SOURCE:

TISSUE TYPE: brain

FEATURE KEY: 5' UTR

IDENTIFICATION METHOD: E

LOCATION: 76..2406

FEATURE KEY: 3' UTR

IDENTIFICATION METHOD: E

a

**SEQUENCE DESCRIPTION:**

5	GCCGAGGCCC GCGCAGTAGC GGTACTAAGT AGAGGCTGCT GGACGCGCCC CACCCGGCAC	60
	CAGGCGGAGC CAGAGATGCT TGCCAGGGCC GAGCGGCCCC GCCCGGGCCC CCGGCCGCCT	120
	CCGGTCTTTC CCTTCCCGCC GCCGCTGTCTG CTGCTGCTGC TGCTGGCGAT ACTAAGCGCC	180
	CCGGTGTGCG GCCGCGTCCC CCGCTCAGTG CCCAGAACCT CGCTGCCCAT CTCCGAGGCT	240
	GACTCCTATC TCACCCGGTT TGCAGCGTCT CATACGTACA ATTACTCTGC TCTCCTTGTG	300
10	GATCCTGCCT CCCACACACT TTACGTCGGT GCACGGGATA GCATCTTCGC TTAAACCCTC	360
	CCCTTCTCTG GGGAAAGACC CCGAAGGATC GACTGGATGG TACCTGAGAC TCACAGACAG	420
	AACTGCAGGA AGAAAGGCAA GAAAGAGGAC GAATGTCACA ATTTTATCCA GATTCTCGCC	480
	ATTGTCAATG CCTCTCACCT CCTCACGTGC GGCACCTTCG CTTTTGATCC GAAGTGCGGG	540
	GTTATTGATG TGTCCAGTTT CCAGCAGGTT GAAAGACTTG ACAGCGGCCG GGGGAAATGT	600
15	CCTTTTGAGC CAGCTCAAACG GTCAGCAGCT GTAATGGCTG GGGGCGTCCT CTACACCGCC	660
	ACTGTGAAGA ACTTCCTGGG GACTGAGCCC ATCATCTCCC GAGCTGTGGG TCGAGCTGAG	720
	GACTGGATTC GAACAGAGAC CTTGTTCATCC TGGCTTAATG CTCCAGCCTT TGTCGCAGCT	780
	ATGGTCCTGA GCCCAGCTGA GTGGGGGGAT GAAGATGGAG ACGATGAAAT CTTTTTTTTT	840
	TTCACGGAGA CCTCCCGAGT GTTGGACTCC TATGAGCGCA TCAAGGTCCC AAGAGTGGCC	900
20	CGAGTGTGTG CGGGGGACCT TGGGGGCAGG AAGACCCTTC AGCAGAGATG GACGACGTTT	960
	CTGAAGGCTG ACCTGCTGTG CCCAGGGCCC GAGCATGCCC GGGCCTCCGG GGTTCCTGCAG	1020
	GCTATGGCAG AGCTTCGGCC TCAGCCTGGA GCGGGAACCC CCATCTTTTA TGGGATCTTT	1080
	TCCTCCCAGT GGGAAGGAGC TGCCATCTCT GCTGTGTGTG CCTTCCGACC CCAAGACATC	1140
	CGGGCAGTGC TGAATGGTCC CTTTAGAGAG CTAAACATG ACTGCAACAG GGGACTGCCT	1200
25	GTCATGGACA ACGAGGTGCC CCAGCCCAGA CCTGGAGAGT GGCATCGCCAA CAACATGAAG	1260

	CTCCAGCAGT	TTGGATCCTC	ACTCTCCCTG	CCAGACCGCG	TGCTCACCTT	TATCAGAGAC	1320
	CACCTCTCA	TGGACAGGCC	CGTGTTCCTG	GCTGACGGCC	GCCCCCTGCT	GGTCACTACA	1380
	GATACAGCCT	ATCTCAGAGT	CGTGGCCAC	AGGGTGACCA	GCCTCTCAGG	GAAAGAATAT	1440
	GACGTGCTCT	ACCTGGGGAC	AGAGGATGGA	CACCTCCACC	GGGCTGTGCG	CATTGAGCT	1500
5	CAGCTCAGTG	TCTTGGAGGA	TCTGGCCTTG	TTCCCAGAAC	CACAGCCGGT	TGAGAGCATG	1560
	AAATTGTACC	ACGATTGGCT	CCTGGTGGGC	TCCCATACTG	AGGTGACACA	AGTGAACACC	1620
	AGCAACTGTG	GCCGTCTCCA	GAGCTGCTCG	GAGTGTATCC	TGGCCCAAGG	CCCCGTGTGC	1680
	GCCTGGAGCT	TCCGGCTTGA	TGCTTGTGTG	GCCCACGCCG	GCGAGCACCG	CGGGATGGTT	1740
	CAAGATATAG	AGTCAGCGGA	TGTCTCTTCT	TTGTGTCCAA	AAGAACCTGG	AGAACATCCC	1800
10	GTAGTGTTTG	AAGTTCCGGT	GGCTACTGTG	GGCCACGTGG	TCCTGCCATG	TTCCCCCAGT	1860
	TCTGCCTGGG	CATCCTGTGT	GTGGCACCAG	CCCAGTGGAG	TGACTGCGCT	CACTCCCCGG	1920
	AGGGATGGAC	TAGAGGTGGT	GGTGACCCCA	GGGGCCTATG	GGGCTTATGC	TTGCGAGTGT	1980
	CAGGAGGGTG	GAGCCGCCCG	CGTGGTGGCT	GCTTATAGCT	TGGTGTGGGG	CAGCCAGCGG	2040
	GGACCCTCAA	ACCGGGCCCA	CACCGTTGTG	GGGGCTGGAT	TGGTTGGCTT	TCTCCTGGGT	2100
15	GTTCTTGCAG	CATCCCTCAC	TCTCCTCCTG	ATTGGTCGCC	GTCAGCAGCG	TCGGCGACAG	2160
	AGGGAGCTTC	TAGCTAGAGA	CAAGGTGGGC	TTAGATCTGG	GGGCTCCACC	TTCTGGGACC	2220
	ACAAGCTATA	GTCAGGACCC	TCCCTCTCCT	TGCGCTGAAG	ATGAACGGCT	GCCCCTGGCC	2280
	CTGGGTAAGC	GGGGCAGTGG	TTTTGGTGGC	TTCCCTCCAC	CCTTCCTGCT	GGATTCTTGC	2340
	CCAAGCCCAG	CCCACATCCG	GCTCACTGGG	GCGCCTCTAG	CCACGTGTGA	TGAGACCTCC	2400
20	ATCTAAAGCC	GGGAAAATG	ACTGCCAGCC	ATGAGCAGTC	TCTGGAACCT	GTGGCTACCA	2460
	AGACCATGAT	CATGGCTGCT	CCTTTCTCTT	GGAGTCTGTG	TGTTACACA	TTAGTGTCTG	2520
	TCCTCTGGAC	CTGGACCTGG	CCTTTGCCCA	GATTCTGAT	TCTCATGAGA	GATCAACCCT	2580
	GTAACCTTCT	GCGATGGCT	CTTGTCTTGG	GCCCATCAGC	TTGTGGGGTG	GAGTAAGGAC	2640
	ATAGGCCCCG	GAAAGGCAAT	CAGTGTGGAG	GAGTTGGGG	CGTGTGTGCC	CTGCGTCCTT	2700
25	GTGGTGGCTG	TATGATTTCC	CAGTCTGCTG	ACTCTGGGGA	GCGCATGATC	CCCTGACTGC	2760

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	CTTGAGATCT CTCCCAACTC AGTTTCCCCT TGCTCTGGAA GAGTGTGTGT CTATACACTG	2820
	GTGTGCCTAG AAGGCCTGTC CATGTGTGCA TGGACGACAG GGCCGGTGCC TCGGTGCTTT	2880
	TGGGGAGTCG GAGAGAAAGG TTGGAATGGG GGACAACTTA ACCCTCGGTA GCCAGTGAGG	2940
	GAAACCACAT GCCCGTCCCC ATCACCCAC AGCGCTTCTT TAACTTTGAG CAAAGTTCCC	3000
5	AAAGTGACCT TCTGGGTGGG AAGGGCAGCA GGACATGTGG CCCCCGTCCT TCTCCTTGTC	3060
	TTTCCCTTCT GGCTGCCAAC CACTGCCGTG CCACCGCTGC GCTTTCCCTG GCTGGAGTGG	3120
	AGGCTGAGTC CTCTGTCCTT GGTTCATT TAAAATGAAC TTCACAACAT TCTAAATATT	3180
	GGGGGATGAC AAATGACTTT TTTCCCCAGA AAAGTGTGTA GGAAATACAA GCAGGTAAAA	3240
	GAAGATTTGC CTCAGTGACT TTCACCCTTG CCCTAAAGCA GGAGTCCCTC AGCTAGCGTC	3300
10	TGTGGACTCC CTGAAATTGT ATGCGTCTGT GGAATCCCTG AAATTGTATG CAAAGTGTCT	3360
	GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT GTTTGCGTGC ATGTGTGCAT	3420
	GTGTGTTTGA TGGCTTTCAT CAGATTCTCA AGGCCTTAAT GAGGTAAAG GACCACGGCC	3480
	TATAGTCACC ACACTTGGGC CACATGGAGG AGGTGTTGCT CTCTGAGGCA GTTCCTCCCT	3540
	GGCCTGCCTG AGGCCAGCCC CTGGACACAT TGCTGCTGGA GACCCACAT CTCTCCAGAA	3600
15	CTTGGAAGCT AGGCTCTGCG CGTGCTTGAA GGCACCACCA TCTCCCTTCT TGCTTCATTC	3660
	TCCTGTGTGC TCTGCCTCTG CTCAGTCCTG CTCTTGGCCT GTGAATGTGC CTCGCCCCGC	3720
	CCTGGTGGGG GACCTCAAAC CCCAGTGCTG ATGCTACCCT TTCCAGTGGG AGTTTCTGTT	3780
	CTGCTTTCCT TGACAGCAGC CTGTGAACTA CTCACGAGTC CCCTTGGTTT GGAGTTCCCG	3840
	GTGGCTTTGA GTAGGATCTT TGGCGTGCCA TCTAACCTAG CAGCATTGAT CGTTCATTGT	3900
20	AAAGTGGGGA TATACCTACC TCAGGGTTGC TGCAAGGATC AAACGAGGAA ACGTATAAAT	3960
	AAAGCATTAC CCACAGCAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	4008

SEQ ID NO: 2

SEQUENCE LENGTH: 2331 base pairs

25 SEQUENCE TYPE: nucleic acid

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STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: No

5 ANTI-SENSE: No

ORIGINAL SOURCE:

ORGANISM: rat (*Rattus norvegicus*)

TISSUE TYPE: brain

FEATURE:

10 FEATURE KEY: CDS

LOCATION: 1..2331

IDENTIFICATION METHOD: E

SEQUENCE DESCRIPTION:

ATGCTTGCCA GGGCCGAGCG GCCCCGCCCG GGCOCOCGGC CGCCTCCGGT CTTTCCCTTC 60  
15 CCGCCGCCGC TGTCGCTGCT GCTGCTGCTG GCGATACTAA GCGCCCCGGT GTGCGGCCGC 120  
GTCCCCCGCT CAGTGCCCAG AACCTCGCTG CCCATCTCCG AGGCTGACTC CTATCTCACC 180  
CGGTTTGAGC CGTCTCATAC GTACAATTAC TCTGCTCTCC TTGTGGATCC TGCCTCCCAC 240  
ACACTTTACG TCGGTGCACG GGATAGCATC TTCGCTTTAA CCCTCCCCTT CTCTGGGGAA 300  
AGACCCCGAA GGATCGACTG GATGGTACCT GAGACTCACA GACAGAACTG CAGGAAGAAA 360  
20 GGCAAGAAAG AGGACGAATG TCACAATTTT ATCCAGATTC TCGCCATTGT CAATGCCTCT 420  
CACCTCTCA CGTGCGGCAC CTTGCTTTT GATCCGAAGT GCGGGGTAT TGATGTGTCC 480  
AGTTTCCAGC AGGTTGAAAG AOTTGAGAGC GGCCGGGGGA AATGTCCTTT TGAGCCAGCT 540  
CAACGGTCAG CAGCTGTAAT GGCTGGGGGC GTCCTCTACA CCGCCACTGT GAAGAACTTC 600  
CTGGGGACTG AGCCCATCAT CTCCGAGCT GTGGGTCGAG CTGAGGACTG GATTCCAACA 660  
25 GAGACCTTGT CATCCTGGCT TAATGCTCCA GCCTTTGTCG CAGCTATGGT CCTGAGCCCA 720

a

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	GCTGAGTGGG GGGATGAAGA TGGAGACGAT GAAATCTTTT TTTTCTTCAC GGAGACCTCC	780
	CGAGTGTTGG ACTCCTATGA GCGCATCAAG GTCCCAAGAG TGGCCCGAGT GTGTGCGGGG	840
	GACCTTGGGG GCAGGAAGAC CCTTCAGCAG AGATGGACGA CGTTTCTGAA GGCTGACCTG	900
	CTGTGCCCAG GGGCCGAGCA TGGCCGGGCC TCCGGGGTTC TGCAGGCTAT GGCAGAGCTT	960
5	CGGCCTCAGC CTGGAGCGGG AACCCCATC TTTTATGGGA TCTTTTCCTC CCAGTGGGAA	1020
	GGAGCTGCCA TCTCTGCTGT GTGTGCCTTC CGACCCCAAG ACATCCGGGC AGTGCTGAAT	1080
	GGTCCCTTTA GAGAGCTAAA ACATGACTGC AACAGGGGAC TGCCTGTCAAT GGACAACGAG	1140
	GTGCCCCAGC CCAGACCTGG AGAGTGCATC GCCAACAACA TGAAGCTCCA GCAGTTTGGA	1200
	TCCTCACTCT CCCTGCCAGA CCGCGTGCTC ACCTTTATCA GAGACCACCC TCTCATGGAC	1260
10	AGGCCCGTGT TCCCGGCTGA CGGCCGCCCC CTGCTGGTCA CTAAGATAC AGCCTATCTC	1320
	AGAGTCGTGG CCCACAGGGT GACCAGCCTC TCAGGGAAAG AATATGACGT GCTCTACCTG	1380
	GGGACAGAGG ATGGACACCT CCACGGGGCT GTGCGCATTG GAGCTCAGCT CAGTGTCTTG	1440
	GAGGATCTGG CCTTGTTCCC AGAACCACAG CCGGTTGAGA GCATGAAATT GTACCACGAT	1500
	TGGCTCCTGG TGGGCTCCCA TACTGAGGTG ACACAAGTGA ACACCAGCAA CTGTGGCCGT	1560
15	CTCCAGAGCT GCTCGGAGTG TATCCTGGCC CAGGACCCCG TGTGCGCCTG GAGCTTCCGG	1620
	CTTGATGCTT GTGTGGCCCA CGCCGGCGAG CACCGCGGGA TGGTTCAAGA TATAGAGTCA	1680
	GCGGATGTCT CTTCTTTGTG TCCAAAAGAA CCTGGAGAAC ATCCCGTAGT GTTTGAAGTT	1740
	CCGGTGGCTA CTGTGGGCCA CGTGGTCCTG CCATGTTCCC CCAGTTCTGC CTGGGCATCC	1800
	TGTGTGTGGC ACCAGCCCAG TGGAGTGAAT GCGCTCACTC CCCGGAGGGA TGGACTAGAG	1860
20	GTGGTGGTGA CCCAGGGGC CATGGGGGCT TATGCTTGCG AGTGTAGGA GGGTGGAGCC	1920
	GCCCCGCTGG TGGCTGCTTA TAGCTTGGTG TGGGGCAGCC AGCGGGGACC CTCAAACCGG	1980
	GCCCACACCG TTGTGGGGGC TGGATTGGTT GGCTTTCTCC TGGGTGTTCT TGCAGCATCC	2040
	CTCACTCTCC TCCTGATTGG TCGCCGTCAG CAGCGTCGGC GACAGAGGGA GCTTCTAGCT	2100
	AGAGACAAGG TGGGCTTAGA TCTGGGGGCT CCACCTTCTG GGACCACAAG CTATAGTCAG	2160
25	GACCCTCCCT CTCCTTCGCC TGAAGATCAA CGGCTGCCCC TGGCCCTGGG TAAGCGGGGC	2220

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AGTGGTTTTG GTGGCTTCCC TCCACCTTC CTGCTGGATT CTTGCCCAAG CCCAGCCCAC 2280

ATCCGGCTCA CTGGGGCGCC TCTAGCCACG TGTGATGAGA CCTCCATCTA A 2331

SEQ ID NO: 3

5 SEQUENCE LENGTH: 776 amino acids

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

10 ORGANISM: rat (*Rattus norvegicus*)

TISSUE TYPE: brain

FEATURE:

FEATURE KEY: peptide

LOCATION: 1..776

15 IDENTIFICATION METHOD: P

SEQUENCE DESCRIPTION:

Met Leu Ala Arg Ala Glu Arg Pro Arg Pro Gly Pro Arg Pro Pro Pro

1 5 10 15

Val Phe Pro Phe Pro Pro Pro Leu Ser Leu Leu Leu Leu Ala Ile

20 20 25 30

Leu Ser Ala Pro Val Cys Gly Arg Val Pro Arg Ser Val Pro Arg Thr

35 40 45

Ser Leu Pro Ile Ser Glu Ala Asp Ser Tyr Leu Thr Arg Phe Ala Ala

50 55 60

25 Ser His Thr Tyr Asn Tyr Ser Ala Leu Leu Val Asp Pro Ala Ser His

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1a

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	65		70		75		80
	Thr	Leu	Tyr	Val	Gly	Ala	Arg
	Asp	Ser	Ile	Phe	Ala	Leu	Thr
	Leu	Pro					
		85		90		95	
	Phe	Ser	Gly	Glu	Arg	Pro	Arg
	Arg	Ile	Asp	Trp	Met	Val	Pro
	Glu	Thr					
5		100		105		110	
	His	Arg	Gln	Asn	Cys	Arg	Lys
	Lys	Gly	Lys	Lys	Glu	Asp	Glu
	Cys	His					
		115		120		125	
	Asn	Phe	Ile	Gln	Ile	Leu	Ala
	Ile	Val	Asn	Ala	Ser	His	Leu
	Leu	Thr					
		130		135		140	
10	Cys	Gly	Thr	Phe	Ala	Phe	Asp
	Pro	Lys	Cys	Gly	Val	Ile	Asp
	Val	Ser					
		145		150		155	
	160						
	Ser	Phe	Gln	Gln	Val	Glu	Arg
	Leu	Glu	Ser	Gly	Arg	Gly	Lys
	Cys	Pro					
		165		170		175	
	Phe	Glu	Pro	Ala	Gln	Arg	Ser
	Ala	Ala	Val	Met	Ala	Gly	Gly
	Val	Leu					
15		180		185		190	
	Tyr	Thr	Ala	Thr	Val	Lys	Asn
	Phe	Leu	Gly	Thr	Glu	Pro	Ile
	Ile	Ser					
		195		200		205	
	Arg	Ala	Val	Gly	Arg	Ala	Glu
	Asp	Trp	Ile	Arg	Thr	Glu	Thr
	Leu	Ser					
		210		215		220	
20	Ser	Trp	Leu	Asn	Ala	Pro	Ala
	Phe	Val	Ala	Ala	Met	Val	Leu
	Ser	Pro					
		225		230		235	
	240						
	Ala	Glu	Trp	Gly	Asp	Glu	Asp
	Gly	Asp	Asp	Glu	Ile	Phe	Phe
	Phe	Phe					
		245		250		255	
	Thr	Glu	Thr	Ser	Arg	Val	Leu
	Asp	Ser	Tyr	Glu	Arg	Ile	Lys
	Val	Pro					
25		260		265		270	

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Arg Val Ala Arg Val Cys Ala Gly Asp Leu Gly Gly Arg Lys Thr Leu

275

280

285

Gln Gln Arg Trp Thr Thr Phe Leu Lys Ala Asp Leu Leu Cys Pro Gly

290

295

300

5 Pro Glu His Gly Arg Ala Ser Gly Val Leu Gln Ala Met Ala Glu Leu

305

310

315

320

Arg Pro Gln Pro Gly Ala Gly Thr Pro Ile Phe Tyr Gly Ile Phe Ser

325

330

335

Ser Gln Trp Glu Gly Ala Ala Ile Ser Ala Val Cys Ala Phe Arg Pro

10

340

345

350

Gln Asp Ile Arg Ala Val Leu Asn Gly Pro Phe Arg Glu Leu Lys His

355

360

365

Asp Cys Asn Arg Gly Leu Pro Val Met Asp Asn Glu Val Pro Gln Pro

370

375

380

15 Arg Pro Gly Glu Cys Ile Ala Asn Asn Met Lys Leu Gln Gln Phe Gly

385

390

395

400

Ser Ser Leu Ser Leu Pro Asp Arg Val Leu Thr Phe Ile Arg Asp His

405

410

415

Pro Leu Met Asp Arg Pro Val Phe Pro Ala Asp Gly Arg Pro Leu Leu

20

420

425

430

Val Thr Thr Asp Thr Ala Tyr Leu Arg Val Val Ala His Arg Val Thr

435

440

445

Ser Leu Ser Gly Lys Glu Tyr Asp Val Leu Tyr Leu Gly Thr Glu Asp

450

455

460

25 Gly His Leu His Arg Ala Val Arg Ile Gly Ala Gln Leu Ser Val Leu

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	465	470	475	480
	Glu Asp Leu Ala Leu Phe Pro Glu Pro Gln Pro Val Glu Ser Met Lys			
	485	490	495	
	Leu Tyr His Asp Trp Leu Leu Val Gly Ser His Thr Glu Val Thr Gln			
5	500	505	510	
	Val Asn Thr Ser Asn Cys Gly Arg Leu Gln Ser Cys Ser Glu Cys Ile			
	515	520	525	
	Leu Ala Gln Asp Pro Val Cys Ala Trp Ser Phe Arg Leu Asp Ala Cys			
	530	535	540	
10	Val Ala His Ala Gly Glu His Arg Gly Met Val Gln Asp Ile Glu Ser			
	545	550	555	560
	Ala Asp Val Ser Ser Leu Cys Pro Lys Glu Pro Gly Glu His Pro Val			
	565	570	575	
	Val Phe Glu Val Pro Val Ala Thr Val Gly His Val Val Leu Pro Cys			
15	580	585	590	
	Ser Pro Ser Ser Ala Trp Ala Ser Cys Val Trp His Gln Pro Ser Gly			
	595	600	605	
	Val Thr Ala Leu Thr Pro Arg Arg Asp Gly Leu Glu Val Val Val Thr			
	610	615	620	
20	Pro Gly Ala Met Gly Ala Tyr Ala Cys Glu Cys Gln Glu Gly Gly Ala			
	625	630	635	640
	Ala Arg Val Val Ala Ala Tyr Ser Leu Val Trp Gly Ser Gln Arg Gly			
	645	650	655	
	Pro Ser Asn Arg Ala His Thr Val Val Gly Ala Gly Leu Val Gly Phe			
25	660	665	670	

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Leu Leu Gly Val Leu Ala Ala Ser Leu Thr Leu Leu Leu Ile Gly Arg

675

680

685

Arg Gln Gln Arg Arg Arg Gln Arg Glu Leu Leu Ala Arg Asp Lys Val

690

695

700

5 Gly Leu Asp Leu Gly Ala Pro Pro Ser Gly Thr Thr Ser Tyr Ser Gln

705

710

715

720

Asp Pro Pro Ser Pro Ser Pro Glu Asp Glu Arg Leu Pro Leu Ala Leu

725

730

735

Gly Lys Arg Gly Ser Gly Phe Gly Gly Phe Pro Pro Pro Phe Leu Leu

10

740

745

750

Asp Ser Cys Pro Ser Pro Ala His Ile Arg Leu Thr Gly Ala Pro Leu

755

760

765

Ala Thr Cys Asp Glu Thr Ser Ile

770

775

15

SEQ ID NO: 4

SEQUENCE LENGTH: 2315 base pairs

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

20 TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: No

ANTI-SENSE: No

ORIGINAL SOURCE:

25 ORGANISM: human (Homo sapiens)

a

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TISSUE TYPE: brain

FEATURE:

FEATURE KEY: CDS

LOCATION: 1..1764

5 IDENTIFICATION METHOD: E

FEATURE KEY: 3' UTR

LOCATION: 1765..2315

IDENTIFICATION METHOD: E

10 SEQUENCE DESCRIPTION:

GGGGGTGTCC TCTATGCTGC CACTGTGAAA AACTACCTGG GGACGGAGCC AATTATCACC 60  
AGAGCAGTGG GTCGTGCCGA GGACTGGATT CGGACAGATA CCTTGCCTTC CTGGCTGAAC 120  
GCCCCAGCCT TTGTCGCAGC CGTGGCCTTG AGCCCAGCCG AATGGGGGGA TGAAGATGGA 180  
GACGACGAAA TCTACTTCTT CTTTACGGAG ACTTCCCGAG CATTTGACTC ATACGAGCGC 240  
15 ATTAAAGTCC CACGGGTGGC CCGTGTGTGT GCGGGGGACC TCGGGGGCCG GAAGACCCTC 300  
CAGCAGAGAT GGACGACGTT TTTGAAAGCT GACCTGCTCT GTCCAGGGCC TGAGCATGGC 360  
CGGGCCTCCA GTGTCCTGCA GGATGTTGCT GTGCTTCGAC CTGAGCTTGG GGCAGGGACT 420  
CCCATCTTTT ATGGCATCTT TTCTTCCCAG TGGGAGGGGG CTAATATCTC TGCTGTCTGT 480  
GCCTTCCGAC CACAAGACAT TCGGACAGTG CTGAATGGTC CCTTCAGAGA ACTAAAACAT 540  
20 GACTGCAACA GAGGACTGCC TGTCGTGGAC AATGATGTGC CCCAGCCCAG ACCTGGAGAG 600  
TGCATCACCA ACAACATGAA GCTCCGGGAC TTTGGCTCAT CTCTCTCCCT GCCTGACCGC 660  
GTACTCACCT TCATCCGGGA CCACCCACTC ATGGACAGGC CAGTGTTTCC AGCTGATGGC 720  
CACCCCTGC TGGTCACTAC AGATACAGCC TATCTCAGAG TCGTGGCCCA CAGGGTGACC 780  
AGCCTCTCAG GGAAAGAGTA TGATGTGCTC TACCTGGGGA CAGAGGATGG ACACCTCCAC 840  
25 CGAGCAGTGC GGATCGGAGC TCAGCTCAGC GTTCTTGAAG ATCTGGCCTT ATTCCCAGAG 900

Q

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CCACAGCCAG TTGAGAACAT GAAATTGTAC CACAGCTGGC TCCTGGTTGG CTCCCGTACT 960  
GAGGTGACAC AAGTGAATAC AACCAACTGT GGCCGTCTCC AGAGCTGCTC AGAGTCCATC 1020  
CTGGCCCAGG ACCCAGTCTG TGCCTGGAGC TTCCGGCTGG ATGAGTGTGT GGCCCATGCC 1080  
GGGGAGCACC GAGGGTTGGT CCAAGACATA GAGTCAGCAG ATGTCTCCTC TTTGTGTCCT 1140  
5 AAAGAGCCTG GAGAACGTCC AGTAGTGTTT GAAGTTCCCG TGGCTACAGC TGCGCATGTG 1200  
GTCTTGCCAT GTTCTCCAAG CTCAGCATGG GCATCCTGTG TGTGGCAGCA GCCCAGTGGA 1260  
GTGACTGCAC TCACCCCCCG GCGGGATGGA CTGGAGGTGG TGGTGACCCC AGGGGCCATG 1320  
GGCGCTTATG CCTGTGAATG TCAGGAGGGT GGGGCAGCCC ATGTGGTAGC AGCTTACAGC 1380  
TTGGTATGGG GCAGCCAGCG AGATGCTCCG AGCCGGGCCC ACACAGTGGG GGCGGGACTG 1440  
10 GCTGGCTTCT TCTTGGGGAT TCTCGCAGCA TCCCTGACTC TCATTCTGAT TGGTCGGCGT 1500  
CAGCAGCGAC GCGGACAGAG GGAACCTCTG GCTAGAGACA AGGTGGGCCT GGACCTGGGG 1560  
GCTCCACCTT CTGGGACCAC AAGCTACAGC CAAGACCCTC CCTCCCCCTC TCCTGAAGAT 1620  
GAGCGGTTGC CGCTGGCCCT GGCCAAGAGG GGCAGTGGCT TTGGTGGATT CTCACCACCC 1680  
TTCCTGCTTG ATCCTTGCCC AAGCCCAGCC CACATTGCGC TAACTGGGGC TCCTCTAGCC 1740  
15 ACATGTGATG AAACATCCAT CTAGAGCTGG GCAAATGACC ACTAGTGAT AAGTGATCAC 1800  
TGGAACGGAG TGACCACTGA GATGCTGGGG GTCAGTGGGC CTGGAAGACC ATCCCAGCCT 1860  
CTGAGTTCTC TTTGAGTATG AGTGATTACT TGGATTTTAG TATCTGTTCT CTCTGAGCCT 1920  
GGATGGGCTT GGGGCCAGAC CTTTGCTGA TTCCTGATTC CCATGAGAAA TCAGAACTGC 1980  
TTTCTGCAGC AAATCAGGGC TTCCCCCTAA CATCTGAACT CCTGTAAACC TTCATCCCTG 2040  
20 GCCCCCTATC TTGGGCCCAT TAGTTTTGGG GATGGGGCAC AGGGCATAGC TATGACTTTG 2100  
CTTCTGGTT GGAGCCTGGC CGGAAGGAAG AGCCCTGGAG GTGGTTGGGG GCAAATGTGC 2160  
CCTGAGTCCT TGGGGTGGTT CTGCTTATTC TTCAAGTTTA TCTGAATCTG TGGGGAGTGC 2220  
ATGATCCCCA TGTTGCAATA TGGAGTCTCT GCCCTGAGAT CTTCCCCTC TCAGTTTTCC 2280  
TTCCATGAAA GAGTACGTGT AAATACATAG TGTTTC 2315

SEQ ID NO: 5

SEQUENCE LENGTH: 1761 base pairs

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

5 TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: No

ANTI-SENSE: No

ORIGINAL SOURCE:

10 ORGANISM: human (Homo sapiens)

TISSUE TYPE: brain

FEATURE:

FEATURE KEY: CDS

LOCATION: 1..1761

15 IDENTIFICATION METHOD: E

SEQUENCE DESCRIPTION:

GGGGGTGTCC TCTATGCTGC CACTGTGAAA AACTACCTGG GGACGGAGCC AATTATCACC 60  
AGAGCAGTGG GTCGTGCCGA GGACTGGATT CGGACAGATA CCTTGCCTTC CTGGCTGAAC 120  
GCCCCAGCCT TTGTCGCAGC CGTGGCCTTG AGCCCAGCCG AATGGGGGGA TGAAGATGGA 180  
20 GACGACGAAA TCTACTTCTT CTTTACGGAG ACTTCCCGAG CATTTGACTC ATACGAGCGC 240  
ATTAAAGTCC CACGGGTGGC CCGTGTGTGT GCGGGGGACC TCGGGGGCCG GAAGACCCTC 300  
CAGCAGAGAT GGACGACGTT TTTGAAAGCT GACCTGCTCT GTCCAGGGCC TGAGCATGGC 360  
CGGGCCTCCA GTGTCCTGCA GGATGTTGCT GTGCTTCGAC CTGAGCTTGG GGCAGGGACT 420  
CCCATCTTTT ATGGCATCTT TTCTTCCCAG TGGGAGGGGG CTAATATCTC TGCTGTCTGT 480  
25 GCCTTCCGAC CACAAGACAT TCGGACAGTG CTGAATGGTC CCTTCAGAGA ACTAAACAT 540

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GACTGCAACA GAGGACTGCC TGTCGTGGAC AATGATGTGC CCCAGCCCAG ACCTGGAGAG 600  
 TGCATCACCA ACAACATGAA GCTCCGGCAC TTTGGCTCAT CTCTCTCCCT GCCTGACCGC 660  
 GTACTCACCT TCATCCGGGA CCACCCACTC ATGGACAGGC CAGTGTTCCT AGCTGATGGC 720  
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SEQ ID NO: 6

SEQUENCE LENGTH: 587 amino acids

25 SEQUENCE TYPE: amino acid



092841801060999

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: human (Homo sapiens)

5 TISSUE TYPE: brain

FEATURE:

FEATURE KEY: peptide

LOCATION: 1..587

IDENTIFICATION METHOD: P

10 SEQUENCE DESCRIPTION:

Gly Gly Val Leu Tyr Ala Ala Thr Val Lys Asn Tyr Leu Gly Thr Glu

5

10

15

Pro Ile Ile Thr Arg Ala Val Gly Arg Ala Glu Asp Trp Ile Arg Thr

20

25

30

15 Asp Thr Leu Pro Ser Trp Leu Asn Ala Pro Ala Phe Val Ala Ala Val

35

40

45

Ala Leu Ser Pro Ala Glu Trp Gly Asp Glu Asp Gly Asp Asp Glu Ile

50

55

60

Tyr Phe Phe Phe Thr Glu Thr Ser Arg Ala Phe Asp Ser Tyr Glu Arg

20

65

70

75

80

Ile Lys Val Pro Arg Val Ala Arg Val Cys Ala Gly Asp Leu Gly Gly

85

90

95

Arg Lys Thr Leu Gln Gln Arg Trp Thr Thr Phe Leu Lys Ala Asp Leu

100

105

110

25 Leu Cys Pro Gly Pro Glu His Gly Arg Ala Ser Ser Val Leu Gln Asp

008748260

a



315

Glu Val Thr Gln Val Asn Thr Thr Asn Cys Gly Arg Leu Gln Ser Cys

325

330

335

Ser Glu Cys Ile Leu Ala Gln Asp Pro Val Cys Ala Trp Ser Phe Arg

340

345

350

5 Leu Asp Glu Cys Val Ala His Ala Gly Glu His Arg Gly Leu Val Gln

355

360

365

Asp Ile Glu Ser Ala Asp Val Ser Ser Leu Cys Pro Lys Glu Pro Gly

370

375

380

Glu Arg Pro Val Val Phe Glu Val Pro Val Ala Thr Ala Ala His Val

10

385

390

395

400

Val Leu Pro Cys Ser Pro Ser Ser Ala Trp Ala Ser Cys Val Trp His

405

410

415

Gln Pro Ser Gly Val Thr Ala Leu Thr Pro Arg Arg Asp Gly Leu Glu

420

425

430

15

Val Val Val Thr Pro Gly Ala Met Gly Ala Tyr Ala Cys Glu Cys Gln

435

440

445

Glu Gly Gly Ala Ala His Val Val Ala Ala Tyr Ser Leu Val Trp Gly

450

455

460

Ser Gln Arg Asp Ala Pro Ser Arg Ala His Thr Val Gly Ala Gly Leu

20

465

470

475

480

Ala Gly Phe Phe Leu Gly Ile Leu Ala Ala Ser Leu Thr Leu Ile Leu

485

490

495

Ile Gly Arg Arg Gln Gln Arg Arg Arg Gln Arg Glu Leu Leu Ala Arg

500

505

510

25

Asp Lys Val Gly Leu Asp Leu Gly Ala Pro Pro Ser Gly Thr Thr Ser

09284180-060999

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Leu Ala Leu Ala Lys Arg Gly Ser Gly Phe Gly Gly Phe Ser Pro Pro  
5 545 550 555 560  
Phe Leu Leu Asp Pro Cys Pro Ser Pro Ala His Ile Arg Leu Thr Gly  
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580 585

10

SEQ ID NO: 7

SEQUENCE LENGTH: 196 base pairs

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

15

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: No

ANTI-SENSE: No

ORIGINAL SOURCE:

20

ORGANISM: human (Homo sapiens)

TISSUE TYPE: brain

FEATURE:

FEATURE KEY: CDS

LOCATION: 1..196

25

IDENTIFICATION METHOD: E

09284180.060999

SEQUENCE DESCRIPTION:

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GCCTGGAGCT TCCGGCTGGA TGAGTGTGTG GCCCATGCCG GGGAGCACCG AGGGTTGGTC 180

5 CAAGACATAG AGTCAG 196

SEQ ID NO: 8

SEQUENCE LENGTH: 30 base pairs

SEQUENCE TYPE: nucleic acid

10 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid, synthetic DNA

HYPOTHETICAL: No

ANTI-SENSE: No

15 SEQUENCE DESCRIPTION:

GATAAGGATC CGGGTCGCCG TCAGCAGCGT 30

SEQ ID NO: 9

SEQUENCE LENGTH: 27 base pairs

20 SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid, synthetic DNA

HYPOTHETICAL: No

25 ANTI-SENSE: Yes

09284180-050999

Q

SEQUENCE DESCRIPTION:

GGCTGGAATT CATTTCCCC GGCTTTA

27

SEQ ID NO: 10

5 SEQUENCE LENGTH: 333 base pairs

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

10 HYPOTHETICAL: No

ANTI-SENSE: No

ORIGINAL SOURCE:

ORGANISM: human (Homo sapiens)

TISSUE TYPE: brain

15 FEATURE:

FEATURE KEY: CDS

LOCATION: 1..333

IDENTIFICATION METHOD: E

SEQUENCE DESCRIPTION:

20 CCCC GCCCGG GTCCCGGCA GCCTACAGCC TCGCCCTTCC CGCTACTGCT GCTGGCGGTG 60  
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TCTGAGGCTG ACTTCTGTCT CACCGGTTC GCAGTCCCTC ACACATACAA TTA CTCTGTT 180  
CTCCTTGTGG ATCCTGCCTC CCACACACTT TATGTTGGCG CCCGGGACAC CATCTTCGCT 240  
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25 CACAGACAGA ACTGTAGGAA GAAAGGCAAG AAA 333

09234130 060999

a

SEQ ID NO: 11

SEQUENCE LENGTH: 111 amino acids

SEQUENCE TYPE: amino acid

5 TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: human (Homo sapiens)

TISSUE TYPE: brain

10 FEATURE:

FEATURE KEY: peptide

LOCATION: 1..111

IDENTIFICATION METHOD: P

SEQUENCE DESCRIPTION:

15 Pro Arg Pro Gly Pro Gly Gln Pro Thr Ala Ser Pro Phe Pro Leu Leu

5

10

15

Leu Leu Ala Val Leu Ser Gly Pro Val Ser Gly Arg Val Pro Arg Ser

20

25

30

Val Pro Arg Thr Ser Leu Pro Ile Ser Glu Ala Asp Phe Cys Leu Thr

20

35

40

45

Arg Phe Ala Val Pro His Thr Tyr Asn Tyr Ser Val Leu Leu Val Asp

50

55

60

Pro Ala Ser His Thr Leu Tyr Val Gly Ala Arg Asp Thr Ile Phe Ala

65

70

75

80

25 Leu Ser Leu Pro Phe Ser Gly Glu Arg Pro Arg Arg Ile Asp Trp Met

09084180 060996

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09284180-060999

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Ala Asp Val Ser Ser Leu Cys Pro Lys Glu Pro Gly Glu His Pro Val  
 565 570 575

Val Phe Glu Val Pro Val Ala Thr Val Gly His Val Val Leu Pro Cys  
 580 585 590

Ser Pro Ser Ser Ala Trp Ala Ser Cys Val Trp His Gln Pro Ser Gly  
 595 600 605

Val Thr Ala Leu Thr Pro Arg Arg Asp Gly Leu Glu Val Val Val Thr  
 610 615 620

Pro Gly Ala Met Gly Ala Tyr Ala Cys Glu Cys Gln Glu Gly Gly Ala  
 625 630 635 640

Ala Arg Val Val Ala Ala Tyr Ser Leu Val Trp Gly Ser Gln Arg Gly  
 645 650 655

Pro Ser Asn Arg Ala His Thr Val Val Gly Ala Gly Leu Val Gly Phe  
 660 665 670

Leu Leu Gly Val Leu Ala Ala Ser Leu Thr Leu Leu Leu Ile Gly Arg  
 675 680 685

Arg Gln Gln Arg Arg Arg Gln Arg Glu Leu Leu Ala Arg Asp Lys Val  
690 695 700

Gly Leu Asp Leu Gly Ala Pro Pro Ser Gly Thr Thr Ser Tyr Ser Gln  
705 710 715 720

Asp Pro Pro Ser Pro Ser Pro Glu Asp Glu Arg Leu Pro Leu Ala Leu  
725 730 735

Gly Lys Arg Gly Ser Gly Phe Gly Gly Phe Pro Pro Pro Phe Leu Leu  
740 745 750

Asp Ser Cys Pro Ser Pro Ala His Ile Arg Leu Thr Gly Ala Pro Leu  
755 760 765

Ala Thr Cys Asp Glu Thr Ser Ile  
770 775

<210> 4

<211> 2315

<212> DNA

<213> Homo sapiens

<220>

<223> Coding region from residue 1 to 1764

<220>

<221> 3'UTR

<222> ()..(2315)

<400> 4

gggggtgtcc tctatgctgc cactgtgaaa aactacctgg ggacggagcc aattatcacc 60  
agagcagtgg gtcgtgccga ggactggatt cggacagata ccttgccttc ctggctgaac 120  
gccccagcct ttgtcgcagc cgtggccttg agcccagccg aatgggggga tgaagatgga 180  
gacgacgaaa tctacttctt ctttacggag acttcccag catttgactc atacgagcgc 240  
attaaagtcc cacgggtggc ccgtgtgtgt gcgggggacc tcggggggcc gaagaccctc 300  
cagcagagat ggacgacgtt tttgaaagct gacctgctct gtccagggcc tgagcatggc 360  
cgggcctcca gtgtcctgca ggatgttgct gtgcttcgac ctgagcttgg ggcagggact 420  
cccatctttt atggcatctt ttcttcccag tgggaggggg ctactatctc tgctgtctgt 480  
gccttccgac cacaagacat tcggacagtg ctgaatggtc ccttcagaga actaaaacat 540  
gactgcaaca gaggactgcc tgtcgtggac aatgatgtgc cccagcccag acctggagag 600  
tgcattacca acaacatgaa gctccggcac tttggctcat ctctctccct gcctgaccgc 660  
gtactcacct tcatccggga ccaccactc atggacaggc cagtgtttcc agctgatggc 720  
caccctctgc tggctactac agatacagcc tatctcagag tcgtggccca cagggtgacc 780  
agcctctcag ggaaagagta tgatgtgctc tacctgggga cagaggatgg acacctccac 840  
cgagcagtgc ggatcggagc tcagctcagc gttcttgaag atctggcctt attcccagag 900

```

ccacagccag ttgagaacat gaaattgtac cacagctggc tcctggttgg ctcccgact 960
gaggtgacac aagtgaatac aaccaactgt ggccgtctcc agagctgctc agagtgcac 1020
ctggcccagg acccagtctg tgccctggagc ttccggctgg atgagtgtgt ggcccatgcc 1080
ggggagcacc gagggtttgt ccaagacata gagtgcagc atgtctcctc tttgtgtcct 1140
aaagagcctg gagaacgtcc agtagtgttt gaagttcccg tggctacagc tgcgcatgtg 1200
gtcttgccat gttctccaag ctacgcatgg gcatcctgtg tgtggcacca gccagtgga 1260
gtgactgcac tcaccccccg gcgggatgga ctggagggtg tggtgacccc aggggccaatg 1320
ggcgcttatg cctgtgaatg tcaggagggt ggggcagccc atgtggtagc agcttacagc 1380
ttggtatggg gcagccagcg agatgctccg agccgggccc acacagtggg gccgggactg 1440
gctggcttct tcttggggat tctgcagca tccctgactc tcattctgat tggtcggcgt 1500
cagcagcgac ggcgacagag ggaacttctg gctagagaca aggtgggcct ggacctggg 1560
gctccacctt ctgggaccac aagctacagc caagaccctc cctccccctc tcctgaagat 1620
gagcggttgc cgctggccct ggccaagagg ggcagtggct ttggtggatt ctcaccaccc 1680
ttcctgcttg atccttgccc aagcccagcc cacattcggc taactggggc tcctctagcc 1740
acatgtgatg aaacatccat ctagagctgg gcaaagacc actagtgtat aagtgatcac 1800
tggaacggag tgaccactga gatgctgggg gtcactgggc ctggaagacc atcccagcct 1860
ctgagttctc tttgagtatg agtgattact tggatttttag tatctgttct ctctgagcct 1920
ggatgggctt ggggcccagc ctttgctga ttcctgattc ccatgagaaa tcagaactgc 1980
tttctgcagc aaatcagggc ttccccctaa catctgaact cctgtaaacc ttcatccctg 2040
gccccctatc ttgggcccct tagttttggg gatggggcac agggcatagc tatgactttg 2100
ctttctgggt ggagcctggc cggaaggaag agccctggag gtggttgggg gcaaagtgtc 2160
cctgagtcct tggggtggtt ctgcttattc ttcaagttta tctgaatctg tggggagtgc 2220
atgatcccca tgttgcaata tggagtctct gccctgagat cttccccatc tcagttttcc 2280
ttccatgaaa gagtacgtgt aaatacatag tgttc 2315

```

<210> 5

<211> 1761

<212> DNA

<213> Homo sapiens

<220>

<223> Coding region from residue 1 to 1761

<400> 5

```

gggggtgtcc tctatgctgc cactgtgaaa aactacctgg ggacggagcc aattatcacc 60
agagcagtgg gtcgtgccga ggactggatt cggacagata ccttgccctc ctggctgaac 120
gccccagcct ttgtgcgagc cgtggccttg agcccagccg aatgggggga tgaagatgga 180
gacgacgaaa tctacttctt ctttacggag acttcccag cathttgactc atacgagcgc 240
attaaagtcc cacgggtggc ccgtgtgtgt gcgggggacc tcggggggccg gaagaccctc 300
cagcagagat ggacgacgtt tttgaaaagc gacctgctct gtccagggcc tgagcatggc 360
cgggcctcca gtgtcctgca ggatgttgct gtgcttcgac ctgagcttgg ggcagggact 420
cccatctttt atggcatctt ttcttcccag tgggaggggg ctactatctc tgctgtctgt 480
gccttccgac cacaagacat tcggacagtg ctgaatggtc ccttcagaga actaaaacat 540
gactgcaaca gaggactgcc tgtcgtggac aatgatgtgc cccagcccag acctggagag 600
tgcataacca acaacatgaa gctccggcac tttggctcat ctctctccct gcctgaccgc 660
gtactcacct tcatccggga ccaccactc atggacaggc cagtgtttcc agctgatggc 720
caccacctgc tggctactac agatacagcc tatctcagag tcgtggccca cagggtgacc 780
agcctctcag ggaaagagta tgatgtgctc tacctgggga cagaggatgg acacctccac 840

```

```

cgagcagtgc ggatcggagc tcagctcagc gttcttgaag atctggcctt attcccagag 900
ccacagccag ttgagaacat gaaattgtac cacagctggc tcctgggttg cccccgtact 960
gaggtgacac aagtgaatac aaccaactgt ggccgtctcc agagctgctc agagtgcac 1020
ctggcccagg acccagctctg tgccctggagc ttccggctgg atgagtgtgt ggcccatgcc 1080
ggggagcacc gagggtttgt ccaagacata gagtcagcag atgtctcctc tttgtgtcct 1140
aaagagcctg gagaacgtcc agtagtgttt gaagttcccg tggctacagc tgcgcatgtg 1200
gtcttgccat gttctccaag ctacagcatgg gcatcctgtg tgtggcacca gccagtgga 1260
gtgactgcac tcaccccccg gcgggatgga ctggaggtgg tggtgacccc aggggccatg 1320
ggcgcttatg cctgtgaatg tcaggagggt ggggcagccc atgtggtagc agcttacagc 1380
ttggtatggg gcagccagcg agatgctccg agccgggccc acacagtggg ggcgggactg 1440
gctggcttct tcttggggat tctgcagca tccctgactc tcattctgat tggtcggcgt 1500
cagcagcgac ggcgacagag ggaacttctg gctagagaca aggtgggcct ggacctggg 1560
gctccacctt ctgggaccac aagctacagc caagaccctc cctccccctc tcctgaagat 1620
gagcggttgc cgctggccct ggccaagagg ggcagtggct ttggtggatt ctaccacccc 1680
ttcctgcttg atccttgccc aagcccagcc cacattcggc taactggggc tcctctagcc 1740
acatgtgatg aaacatccat c 1761

```

```

<210> 6
<211> 587
<212> PRT
<213> Homo sapiens

```

```

<400> 6
Gly Gly Val Leu Tyr Ala Ala Thr Val Lys Asn Tyr Leu Gly Thr Glu
 1             5             10            15

Pro Ile Ile Thr Arg Ala Val Gly Arg Ala Glu Asp Trp Ile Arg Thr
      20             25            30

Asp Thr Leu Pro Ser Trp Leu Asn Ala Pro Ala Phe Val Ala Ala Val
      35             40            45

Ala Leu Ser Pro Ala Glu Trp Gly Asp Glu Asp Gly Asp Asp Glu Ile
      50             55            60

Tyr Phe Phe Phe Thr Glu Thr Ser Arg Ala Phe Asp Ser Tyr Glu Arg
      65             70            75            80

Ile Lys Val Pro Arg Val Ala Arg Val Cys Ala Gly Asp Leu Gly Gly
      85             90            95

Arg Lys Thr Leu Gln Gln Arg Trp Thr Thr Phe Leu Lys Ala Asp Leu
      100            105            110

Leu Cys Pro Gly Pro Glu His Gly Arg Ala Ser Ser Val Leu Gln Asp
      115            120            125

Val Ala Val Leu Arg Pro Glu Leu Gly Ala Gly Thr Pro Ile Phe Tyr

```



130	135	140
Gly Ile Phe Ser Ser Gln Trp Glu Gly Ala Thr Ile Ser Ala Val Cys		
145	150	155 160
Ala Phe Arg Pro Gln Asp Ile Arg Thr Val Leu Asn Gly Pro Phe Arg		
	165	170 175
Glu Leu Lys His Asp Cys Asn Arg Gly Leu Pro Val Val Asp Asn Asp		
	180	185 190
Val Pro Gln Pro Arg Pro Gly Glu Cys Ile Thr Asn Asn Met Lys Leu		
	195	200 205
Arg His Phe Gly Ser Ser Leu Ser Leu Pro Asp Arg Val Leu Thr Phe		
	210	215 220
Ile Arg Asp His Pro Leu Met Asp Arg Pro Val Phe Pro Ala Asp Gly		
	225	230 235 240
His Pro Leu Leu Val Thr Thr Asp Thr Ala Tyr Leu Arg Val Val Ala		
	245	250 255
His Arg Val Thr Ser Leu Ser Gly Lys Glu Tyr Asp Val Leu Tyr Leu		
	260	265 270
Gly Thr Glu Asp Gly His Leu His Arg Ala Val Arg Ile Gly Ala Gln		
	275	280 285
Leu Ser Val Leu Glu Asp Leu Ala Leu Phe Pro Glu Pro Gln Pro Val		
	290	295 300
Glu Asn Met Lys Leu Tyr His Ser Trp Leu Leu Val Gly Ser Arg Thr		
	305	310 315 320
Glu Val Thr Gln Val Asn Thr Thr Asn Cys Gly Arg Leu Gln Ser Cys		
	325	330 335
Ser Glu Cys Ile Leu Ala Gln Asp Pro Val Cys Ala Trp Ser Phe Arg		
	340	345 350
Leu Asp Glu Cys Val Ala His Ala Gly Glu His Arg Gly Leu Val Gln		
	355	360 365
Asp Ile Glu Ser Ala Asp Val Ser Ser Leu Cys Pro Lys Glu Pro Gly		
	370	375 380
Glu Arg Pro Val Val Phe Glu Val Pro Val Ala Thr Ala Ala His Val		

385		390		395		400									
Val	Leu	Pro	Cys	Ser	Pro	Ser	Ser	Ala	Trp	Ala	Ser	Cys	Val	Trp	His
				405					410					415	
Gln	Pro	Ser	Gly	Val	Thr	Ala	Leu	Thr	Pro	Arg	Arg	Asp	Gly	Leu	Glu
			420					425					430		
Val	Val	Val	Thr	Pro	Gly	Ala	Met	Gly	Ala	Tyr	Ala	Cys	Glu	Cys	Gln
			435					440				445			
Glu	Gly	Gly	Ala	Ala	His	Val	Val	Ala	Ala	Tyr	Ser	Leu	Val	Trp	Gly
	450						455				460				
Ser	Gln	Arg	Asp	Ala	Pro	Ser	Arg	Ala	His	Thr	Val	Gly	Ala	Gly	Leu
465					470					475					480
Ala	Gly	Phe	Phe	Leu	Gly	Ile	Leu	Ala	Ala	Ser	Leu	Thr	Leu	Ile	Leu
				485					490					495	
Ile	Gly	Arg	Arg	Gln	Gln	Arg	Arg	Arg	Gln	Arg	Glu	Leu	Leu	Ala	Arg
				500				505					510		
Asp	Lys	Val	Gly	Leu	Asp	Leu	Gly	Ala	Pro	Pro	Ser	Gly	Thr	Thr	Ser
		515					520					525			
Tyr	Ser	Gln	Asp	Pro	Pro	Ser	Pro	Ser	Pro	Glu	Asp	Glu	Arg	Leu	Pro
	530					535					540				
Leu	Ala	Leu	Ala	Lys	Arg	Gly	Ser	Gly	Phe	Gly	Gly	Phe	Ser	Pro	Pro
545					550					555					560
Phe	Leu	Leu	Asp	Pro	Cys	Pro	Ser	Pro	Ala	His	Ile	Arg	Leu	Thr	Gly
				565					570					575	
Ala	Pro	Leu	Ala	Thr	Cys	Asp	Glu	Thr	Ser	Ile					
			580					585							

<210> 7

<211> 196

<212> DNA

<213> Homo sapiens

<220>

<223> Coding region from residue 1 to 196

<400> 7

```

aaattgtacc acagctggct cctggttggc tcccgtactg aggtgacaca agtgaataca 60
accaactgtg gccgtctcca gagctgctca gagtgcattc tggcccagga cccagtctgt 120
gcctggagct tccggctgga tgagtgtgtg gcccatgccg gggagcaccg aggggttggtc 180
caagacatag agtcag                                     196

```

```

<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Synthetic DNA

```

```

<400> 8
gataaggatc cgggtcgccg tcagcagcgt                                     30

```

```

<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Synthetic DNA

```

```

<400> 9
ggctggaatt cattttcccc ggcttta                                     27

```

```

<210> 10
<211> 333
<212> DNA
<213> Homo sapiens

```

```

<220>
<223> Coding region from residue 1 to 333

```

```

<400> 10
ccccggccgg gtcccgggca gcctacagcc tcgcccttcc cgctactgct gctggcggtg 60
ctgagcggcc cggatatccg ccgcgtcccc cgctcggtgc ccagaacctc gcttccaatc 120
tctgaggctg acttctgtct caccgggttc gcagtccttc acacatacaa ttactctgtt 180
ctccttgtgg atcctgcctc ccacacactt tatgttggcg cccgggacac catcttcgct 240
ttatccctgc ccttctcagg ggagagaccc cgcaggattg actggatggt tcctgaggct 300
cacagacaga actgtaggaa gaaaggcaag aaa                                     333

```

```

<210> 11
<211> 111
<212> PRT
<213> Homo sapiens

```

<400> 11

Pro Arg Pro Gly Pro Gly Gln Pro Thr Ala Ser Pro Phe Pro Leu Leu  
1 5 10 15

Leu Leu Ala Val Leu Ser Gly Pro Val Ser Gly Arg Val Pro Arg Ser  
20 25 30

Val Pro Arg Thr Ser Leu Pro Ile Ser Glu Ala Asp Phe Cys Leu Thr  
35 40 45

Arg Phe Ala Val Pro His Thr Tyr Asn Tyr Ser Val Leu Leu Val Asp  
50 55 60

Pro Ala Ser His Thr Leu Tyr Val Gly Ala Arg Asp Thr Ile Phe Ala  
65 70 75 80

Leu Ser Leu Pro Phe Ser Gly Glu Arg Pro Arg Arg Ile Asp Trp Met  
85 90 95

Val Pro Glu Ala His Arg Gln Asn Cys Arg Lys Lys Gly Lys Lys  
100 105 110

<210> 12

<211> 7

<212> PRT

<213> Homo sapiens

<400> 12

Gln Asp Pro Val Cys Ala Trp  
1 5

<210> 13

<211> 6

<212> PRT

<213> Homo sapiens

<220>

<223> First Xaa = Gln or Arg

<220>

<223> Second Xaa = Ala or Gly

<400> 13

Xaa Asp Tyr Cys Xaa Trp  
1 5

<210> 14

<211> 14

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: Myc tag

<400> 14

Asp Ile Gly Gly Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu

1

5

10